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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/997,137

DATE: 12/13/2001
 TIME: 14:04:51

Input Set : A:\79-00.app
 Output Set: N:\CRF3\12132001\I997137.raw

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C--> 3 <110> APPLICANT: Summers, Anne O.
 4 Caguiat, Jonathan
 6 <120> TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
 7 Methods
 9 <130> FILE REFERENCE: 79-00
 11 <140> CURRENT APPLICATION NUMBER: US/09/997,137
 12 <141> CURRENT FILING DATE: 2001-10-12
 14 <150> PRIOR APPLICATION NUMBER: US 60/240,465
 15 <151> PRIOR FILING DATE: 2000-10-12
 17 <160> NUMBER OF SEQ ID NOS: 18
 19 <170> SOFTWARE: PatentIn Ver. 2.0
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 22 <211> LENGTH: 435
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Shigella flexneri, Tn21 of Plasmid R100
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 29 ggcagcatcc gccgctatgg ggaggcggac gtgggttcggg tgaaattcgt gaaatcggca 180
 30 cagcggctgg ggttcagtct ggacgagatt gccgagctgt tgcggctcga cgatggcacc 240
 31 cactgcgagg aggccagcag cctggccgaa cacaagctca aggacgtgcg cgagaagatg 300
 32 gccgacttgg cgcgcatgga aaccgtgctg tctgaactcg tgtgcgctg ccatgcacga 360
 33 aaggggaatg tttcctgccc gttgatcgcg tcactacagg gcgaagcagg cctggcaagg 420
 34 tcagctatgc cttag 435
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 37 <211> LENGTH: 144
 38 <212> TYPE: PRT
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 42 Met Glu Asn Asn Leu Glu Asn Leu Thr Ile Gly Val Phe Ala Lys Ala
 43 1 5 10 15
 45 Ala Gly Val Asn Val Glu Thr Ile Arg Phe Tyr Gln Arg Lys Gly Leu
 46 20 25 30
 48 Leu Arg Glu Pro Asp Lys Pro Tyr Gly Ser Ile Arg Arg Tyr Gly Glu
 49 35 40 45
 51 Ala Asp Val Val Arg Val Lys Phe Val Lys Ser Ala Gln Arg Leu Gly
 52 50 55 60
 54 Phe Ser Leu Asp Glu Ile Ala Glu Leu Leu Arg Leu Asp Asp Gly Thr
 55 65 70 75 80
 57 His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val
 58 85 90 95
 60 Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu
 61 100 105 110
 63 Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Leu
 64 115 120 125
 66 Ile Ala Ser Leu Gln Gly Glu Ala Gly Leu Ala Arg Ser Ala Met Pro
 67 130 135 140

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79 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
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84 gcacgaaagg ggaatgtttc ctgcccgttg atcgcgtcac tacagggatc ctcaggcacc 180
85 cactgcgagg aggccagcag cctggccgaa cacaagctca aggacgtgcg cgagaagatg 240
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101 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
102 20 25 30
104 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
105 35 40 45
107 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
108 50 55 60
110 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
111 65 70 75 80
113 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
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116 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
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119 Pro Gln Phe Glu Lys
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129 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
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135 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
136 20 25 30
138 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
139 35 40 45

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141 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
142      50                      55                      60
144 Val Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
145 65                      70                      75                      80
147 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
148                      85                      90                      95
150 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
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153 Pro Gln Phe Glu Lys
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162 <220> FEATURE:
163 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
165 <400> SEQUENCE: 6
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167 1      5                      10                      15
169 Asp Val Arg Glu Lys Thr Met Ala Asp Leu Ala Arg Met Glu Thr Val
170      20                      25                      30
172 Leu Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser
173      35                      40                      45
175 Cys Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu
176      50                      55                      60
178 Glu Ala Ser Ser Leu Val Glu His Lys Leu Lys Asp Val Arg Glu Lys
179 65                      70                      75                      80
181 Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys
182                      85                      90                      95
184 Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser
185      100                      105                      110
187 His Pro Gln Phe Glu Lys
188      115
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192 <211> LENGTH: 117
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial Sequence
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197 <223> OTHER INFORMATION: Description of Artificial Sequence: chelon
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201 1      5                      10                      15
203 Asp Val Arg Glu Thr Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
204      20                      25                      30
206 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
207      35                      40                      45
209 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
210      50                      55                      60
212 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Thr Met

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213   65                               70                               75                               80
215 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
216                               85                               90                               95
218 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
219                               100                               105                               110
221 Pro Gln Phe Glu Lys
222                               115
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227 <212> TYPE: PRT
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230 <220> FEATURE:
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233 <400> SEQUENCE: 8
234 Met Thr His Cys Glu Glu Ala Ser Ser Leu Ala Glu His Lys Leu Lys
235   1                               5                               10                               15
237 Asp Val Arg Glu Gln Met Ala Asp Leu Ala Arg Met Glu Thr Val Leu
238                               20                               25                               30
240 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
241                               35                               40                               45
243 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
244   50                               55                               60
246 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Gln Met
247   65                               70                               75                               80
249 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
250                               85                               90                               95
252 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
253                               100                               105                               110
255 Pro Gln Phe Glu Lys
256                               115
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260 <211> LENGTH: 117
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262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
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267 <400> SEQUENCE: 9
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271 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Val Glu Thr Val Leu
272                               20                               25                               30
274 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
275                               35                               40                               45
277 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
278   50                               55                               60
280 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
281   65                               70                               75                               80
283 Ala Asp Leu Ala Arg Val Glu Thr Val Leu Ser Glu Leu Val Cys Ala
284                               85                               90                               95

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289 Pro Gln Phe Glu Lys
290           115
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301 <400> SEQUENCE: 10
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303   1           5           10           15
305 Asp Val Arg Glu Lys Met Ala Asp Leu Ala Arg Ile Glu Thr Val Leu
306           20           25           30
308 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Ser Cys
309           35           40           45
311 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
312           50           55           60
314 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
315   65           70           75           80
317 Ala Asp Leu Ala Arg Ile Glu Thr Val Leu Ser Glu Leu Val Cys Ala
318           85           90           95
320 Cys His Ala Arg Lys Gly Asn Val Ser Cys Pro Ser Ala Trp Ser His
321           100           105           110
323 Pro Gln Phe Glu Lys
324           115
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337   1           5           10           15
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340           20           25           30
342 Ser Glu Leu Val Cys Ala Cys His Ala Arg Lys Gly Asn Val Pro Cys
343           35           40           45
345 Pro Leu Ile Ala Ser Leu Gln Gly Ser Ser Gly Thr His Cys Glu Glu
346           50           55           60
348 Ala Ser Ser Leu Ala Glu His Lys Leu Lys Asp Val Arg Glu Lys Met
349   65           70           75           80
351 Ala Asp Leu Ala Arg Met Glu Thr Val Leu Ser Glu Leu Val Cys Ala
352           85           90           95
354 Cys His Ala Arg Lys Gly Asn Val Pro Cys Pro Ser Ala Trp Ser His
355           100           105           110
357 Pro Gln Phe Glu Lys

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VERIFICATION SUMMARY

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